



#4

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The Regents of the University of California

<120> Use of Insect Cell Membrane Transporters as Novel
Target Sites for Insecticides

<130> 023070-093800US

<140> US 09/815,923

<141> 2001-03-23

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<170> PatentIn Ver. 2.1

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<210> 6

<211> 556

<212> PRT

<213> Manduca sexta

<220>

<223> proline transporter

<400> 6

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Met Ser Gly Ala Thr Gln Asp Arg Trp Gly Ser Gln Leu Glu Tyr Leu
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Leu Ser Cys Leu Gly Tyr Ala Val Gly Ile Gly Asn Leu Trp Arg Phe
          20             25             30

Pro Tyr Leu Cys Tyr Arg Asn Gly Gly Gly Ala Phe Leu Ile Pro Tyr
      35             40             45

Phe Leu Thr Leu Ile Ile Cys Gly Ile Pro Leu Val Tyr Leu Glu Thr
      50             55             60

Thr Leu Gly Gln Phe Ala Ser Ala Gly Cys Ile Ser Val Phe Asn Ile
      65             70             75             80

Asn Pro Leu Phe Lys Gly Ala Gly Tyr Ala Val Ile Val Leu Asn Val
          85             90             95

Ile Ala Ser Ile Tyr Phe Ser Ala Ile Met Ser Tyr Pro Ile Leu Tyr
      100            105            110

Ile Tyr His Ser Met Ser Ser Pro Leu Pro Trp Gln Ser Cys Gly Asn
      115            120            125

```


Ser	Trp	Asn	Thr	Val	Asn	Cys	Thr	Glu	Ile	Thr	Gly	Asn	Ser	Ser	Phe	
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Arg	His	Leu	Leu	Gln	Val	Ser	Pro	Asn	Ile	Asn	His	Ile	Gly	Ser	Ile	
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Val	Ala	Pro	Val	Phe	Trp	Cys	Asn	Leu	Ile	Cys	Trp	Ile	Leu	Val	Tyr	
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Leu	Cys	Ile	Cys	Asn	Gly	Val	Lys	Ser	Val	Gly	Lys	Ile	Val	Tyr	Phe	
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Thr	Val	Leu	Phe	Pro	Tyr	Val	Val	Leu	Ser	Val	Leu	Phe	Val	Arg	Gly	
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Ile	Thr	Leu	Pro	Gly	Ala	Trp	Lys	Gly	Ile	Met	Phe	Tyr	Ile	Leu	Pro	
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Asp	Trp	Ala	Gln	Leu	Ala	Lys	Pro	Lys	Val	Trp	Ala	Asp	Ala	Ala	Thr	
			245						250					255		
Gln	Ile	Phe	Phe	Ser	Leu	Gly	Pro	Gly	Trp	Gly	Gly	Leu	Val	Ser	Met	
		260						265					270			
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Phe	Ser	Val	Leu	Gly	Phe	Ala	Ala	Glu	Arg	Thr	Asn	Val	Pro	Val	Ser	
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Gln	Val	Ala	Thr	Ala	Gly	Pro	Gly	Leu	Ala	Phe	Val	Thr	Tyr	Pro	Ala	
				325					330					335		
Thr	Val	Thr	Met	Met	Pro	Ala	Pro	Asn	Leu	Trp	Ala	Ile	Thr	Phe	Phe	
			340					345					350			
Val	Met	Leu	Phe	Phe	Leu	Gly	Ile	Asp	Thr	Met	Phe	Val	Thr	Ile	Glu	
	355						360					365				
Ala	Ile	Ile	Ala	Gly	Leu	Leu	Asp	Glu	Phe	Pro	Arg	Phe	Lys	Ser	Arg	
	370					375					380					
Lys	Arg	Ile	Ile	Ala	Phe	Ile	Thr	Cys	Val	Val	Leu	Phe	Ser	Phe	Ser	
385					390					395					400	
Ile	Ile	Cys	Asn	Thr	Glu	Gly	Gly	Leu	His	Val	Ile	Gly	Leu	Leu	Asp	
			405						410					415		
Ser	His	Val	Ala	Ile	Leu	Cys	Val	Pro	Leu	Val	Cys	Ala	Leu	Glu	Ile	
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	435						440					445				

Met Thr Gly Arg Pro Leu Arg Arg Ile Trp Met Val Leu Trp Arg Tyr
450 455 460

Val Ile Leu Leu Ile Leu Leu Val Ile Thr Leu Tyr Ser Leu Leu Glu
465 470 475 480

Val Ser Ser Leu Ala Gly Trp Phe Ile Thr Leu Val Ser Val Val Cys
485 490 495

Ile Pro Ile Tyr Ala Ala Lys Val Leu Leu Arg Ala Glu Gly Ser Leu
500 505 510

Leu Glu Arg Ile Arg Ala Ser Cys Arg Pro Ser Asn Asp Trp Gly Pro
515 520 525

Ser Glu Pro Glu Lys Arg Arg Glu Trp Glu Leu Leu Lys Lys Gln Lys
530 535 540

Ala Asp Ile Phe Pro Leu Asn Asp Leu Asp Lys Tyr
545 550 555

<210> 7
<211> 1995
<212> DNA
<213> Aedes aegypti

<220>
<223> glutamate transporter

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<210> 8
<211> 481
<212> PRT
<213> Aedes aegypti

<220>
<223> glutamate transporter

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Leu Arg Glu Val Pro Ala Glu Gly Glu Lys Trp Thr Ala Arg Asp Val
35 40 45
Ala Tyr Ile Asn Phe Val Gly Asp Ile Phe Leu Arg Met Leu Lys Ala
50 55 60
Leu Ile Leu Pro Leu Ile Val Thr Ser Leu Ile Ala Ala Val Gly Ser
65 70 75 80
Leu Asp Leu Ser Leu Ser Gly Lys Ile Gly Gly Arg Ala Val Leu Tyr
85 90 95
Tyr Val Ile Thr Thr Val Met Ala Val Ile Leu Gly Ile Val Leu Val
100 105 110
Val Thr Ile Gln Pro Gly Lys Gly Ala Glu Glu Thr Ser Gly Ala Val
115 120 125
Lys Gly Glu Val Arg Asn Val Thr Thr Ala Asp Thr Leu Leu Asp Leu
130 135 140
Val Arg Asn Met Phe Pro Pro Asn Leu Val Gln Ala Cys Leu Gln Gln
145 150 155 160
Tyr Gln Thr Val Leu Thr Pro Pro Lys Ser Asn Pro Val Glu Thr Asp
165 170 175
Leu Ile Leu Trp Ser Val Gly Gly Lys Phe Val Asp Gly Met Asn Ile
180 185 190
Ile Gly Leu Val Val Ala Ser Ile Val Phe Gly Ile Ala Leu Gly Ala
195 200 205
Leu Lys Glu Asp Val Gln Leu Val Leu Lys Phe Phe Gln Gln Leu Ser
210 215 220
His Thr Ile Met Lys Val Thr Gly Trp Val Ile Trp Leu Ser Pro Ile
225 230 235 240

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<210> 10

<211> 727

<212> PRT

<213> Manduca sexta

<220>

<223> neurotransmitter transporter encoded by inebriated
gene

<400> 10

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Met Asn Lys Val Glu Ser Ser Thr Glu Ala Ala Ala Pro Ser Val Ala
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Ile His Val Glu Gln His Asp Asp Glu Gln Asp Lys Glu Asn Ser Lys
      20                      25                      30

```

```

Leu Leu Ser Ala His Ser Pro Ala Pro Ser Ile Thr Pro Ser Gly Gln
      35                      40                      45

```

```

Met Arg Lys Val Lys Ser Phe Ser Asp Thr His Lys Ile Arg Asp Val
      50                      55                      60

```

```

Thr Thr Ala Ser Gly Ala Ala Ser Ala Arg Ser Leu Arg Pro Tyr Glu
      65                      70                      75                      80

```

```

Ile Val Asn Thr Tyr Pro Glu Gly Ser Glu Ser Gly Thr Asn Asn Tyr
      85                      90                      95

```

```

Gly Ala Pro Ser Val Arg Ser Leu Ala Ser Ile Gly Met Gly Cys Thr
      100                      105                      110

```

```

Asp Gly Arg Lys Met Val Ile Arg Arg Val Pro Thr Ser Pro Thr Glu
      115                      120                      125

```

```

Leu Phe His Leu Val Arg Pro Pro Thr Pro Pro Asp Glu Asp Ser Ala
      130                      135                      140

```

```

Ser His Glu Ser Asp Cys Glu Glu Glu Glu Glu Asp Ala Ala Val His
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```

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 Ala Cys Val Gly Tyr Ser Val Gly Leu Gly Asn Val Trp Arg Phe Pro
 180 185 190
 Tyr Leu Cys Tyr Lys Ser Gly Gly Gly Ala Phe Leu Ile Pro Tyr Phe
 195 200 205
 Ile Ile Leu Leu Ile Cys Gly Val Pro Met Leu Phe Met Glu Leu Ala
 210 215 220
 Ile Gly Gln Tyr Thr Ala His Gly Pro Ile Gly Ala Leu Ser Gln Ile
 225 230 235 240
 Cys Pro Leu Phe Lys Gly Ala Gly Leu Ala Ser Val Val Ile Ser Phe
 245 250 255
 Leu Met Ser Thr Tyr Tyr Ala Val Ile Ile Ala Trp Ala Ile Tyr Tyr
 260 265 270
 Phe Phe Thr Ser Phe Lys Thr Glu Val Pro Trp Ala Ser Cys Ser Asn
 275 280 285
 Arg Trp Asn Thr Asp Gln Cys Trp Val Pro Asn His Asn His Thr Lys
 290 295 300
 Pro Asn Gly Ser Gln Thr Pro Thr Glu Gln Phe Phe Glu Arg Lys Val
 305 310 315 320
 Leu Asn Met Ser Ala Gly Ile Glu Tyr Pro Gly Gly Met Arg Trp Glu
 325 330 335
 Leu Ala Ala Cys Leu Val Cys Ala Trp Val Leu Val Tyr Phe Ala Leu
 340 345 350
 Trp Lys Ser Ile Lys Ser Ser Ala Lys Val Arg Tyr Ile Thr Thr Thr
 355 360 365
 Leu Pro Phe Leu Leu Ile Ile Val Phe Leu Gly Arg Ser Leu Thr Leu
 370 375 380
 Asp Gly Ala Asp Gly Gly Leu Arg Phe Phe Phe Lys Pro Asp Trp Glu
 385 390 395 400
 Leu Leu Lys Gln Ser Arg Pro Trp Val Asn Ala Ala Ser Gln Ile Phe
 405 410 415
 Asn Ser Ile Gly Ile Ala Phe Gly Ser Met Ile Met Phe Ala Ser Tyr
 420 425 430
 Asn Arg Phe Asp Asn Asn Phe Leu His Asp Thr Val Ala Val Thr Leu
 435 440 445
 Val Asn Ala Ile Thr Ser Leu Ile Val Gly Ile Phe Thr Phe Ala Thr
 450 455 460
 Ile Gly Asn Ile Ala Phe Glu Gln Asn Thr Pro Val Lys Asp Val Ile
 465 470 475 480

Ala	Asp	Ser	Pro	Gly	Leu	Leu	Phe	Val	Val	Tyr	Pro	Gln	Ala	Ile	Ala
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Lys	Met	Pro	Ala	Ser	Gln	Leu	Trp	Ala	Val	Leu	Phe	Phe	Phe	Met	Phe
			500					505					510		
Leu	Cys	Leu	Gly	Leu	Asn	Ser	Gln	Phe	Ala	Ile	Val	Glu	Val	Val	Val
		515					520					525			
Thr	Ser	Ile	Gln	Asp	Gly	Phe	Pro	Asp	Met	Ile	Arg	Lys	Arg	Leu	Val
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Tyr	His	Glu	Leu	Leu	Val	Leu	Leu	Val	Cys	Ala	Val	Ser	Leu	Leu	Cys
545					550					555					560
Gly	Leu	Pro	His	Ile	Ile	His	Ser	Gly	Ile	Tyr	Val	Phe	Gln	Leu	Met
				565					570					575	
Asp	Tyr	Tyr	Ala	Ala	Ser	Leu	Ser	Ile	Thr	Tyr	Leu	Ala	Phe	Phe	Glu
			580					585					590		
Val	Val	Ala	Ile	Ala	Trp	Phe	Tyr	Gly	Val	Gly	Arg	Leu	Ser	Arg	Asn
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Ile	Lys	Gln	Met	Thr	Gly	Arg	Gln	Pro	Ser	Leu	Tyr	Phe	Arg	Phe	Cys
	610					615					620				
Trp	Leu	Ile	Ala	Ser	Pro	Ala	Leu	Leu	Leu	Ala	Leu	Trp	Val	Ala	Ser
625					630					635					640
Met	Val	Asp	Tyr	Thr	Pro	Pro	Ser	Tyr	Arg	Gln	Tyr	Gln	Tyr	Pro	Ala
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Trp	Ala	Gln	Ala	Leu	Gly	Trp	Ile	Met	Ala	Ser	Leu	Ser	Leu	Leu	Cys
			660					665					670		
Ile	Pro	Val	Tyr	Ala	Val	Ile	Val	Ile	Ile	Arg	Ala	Pro	Gly	Asp	Ser
		675					680					685			
Leu	Arg	Glu	Lys	Leu	Arg	Tyr	Ser	Ile	Gln	Pro	Thr	Ser	Ile	Cys	Glu
	690					695					700				
Cys	Gly	Val	Asn	Gly	Cys	Asp	Ile	Cys	Cys	Ser	Glu	Ser	Asp	Pro	Pro
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Asp	Asp	Lys	Thr	Val	Ile	Asn									
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<210> 11
 <211> 2034
 <212> DNA
 <213> Manduca sexta

<220>
 <223> orphan transporter

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 gggctccttg aacgtgatgc tcctgaggaa gaccgcgctg cgtggtcagg gaagctccag 180


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<210> 12
<211> 676
<212> PRT
<213> Manduca sexta

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<220>
<223> orphan transporter

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Ala Pro Leu Thr Thr Arg Ser Asp Gly Ser Glu Arg Pro His Gly Val
          20             25             30

Thr Ile Val Leu Gln Gly Ser Arg Gly Ser Leu Gln Arg Asp Ala Pro
  35             40             45

Glu Glu Asp Arg Ala Ala Trp Ser Gly Lys Leu Gln Phe Phe Leu Ser
  50             55             60

Ile Ile Gly Tyr Ser Val Gly Leu Gly Asn Ile Trp Arg Phe Pro Tyr
  65             70             75             80

Leu Cys Gln Gln Asn Gly Gly Gly Ala Phe Leu Ile Pro Phe Leu Ile
          85             90             95

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Met	Leu	Val	Leu	Glu	Gly	Ile	Pro	Leu	Val	Leu	Ile	Glu	Met	Ala	Ile		
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Gly	Gln	Lys	Met	Arg	Leu	Gly	Ser	Leu	Gly	Val	Trp	Asn	Thr	Ile	His		
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Pro	Trp	Leu	Gly	Gly	Ile	Gly	Ile	Ser	Ser	Cys	Val	Val	Thr	Leu	Phe		
	130					135					140						
Val	Ala	Leu	Tyr	Tyr	Asn	Val	Ile	Ile	Thr	Trp	Val	Phe	Phe	Tyr	Leu		
145					150					155					160		
Phe	Asn	Ser	Ile	Arg	Leu	Thr	Ala	Asp	Gln	Leu	Pro	Trp	Ala	His	Cys		
				165					170					175			
Pro	Tyr	Asp	Asn	Gly	Thr	Ala	Glu	Ala	Glu	Cys	Asn	Lys	Ala	Ser	Ala		
			180					185					190				
Thr	Val	Tyr	Phe	Trp	Tyr	Arg	Glu	Ala	Leu	Asp	Ala	Ser	Pro	Ser	Ile		
	195						200					205					
Asp	Glu	Pro	Gly	Val	Pro	Arg	Trp	Trp	Ile	Val	Leu	Tyr	Leu	Leu	Leu		
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Ala	Trp	Ile	Ile	Val	Phe	Phe	Ile	Val	Met	Lys	Gly	Ile	Gln	Ser	Ser		
225					230					235					240		
Gly	Lys	Val	Val	Tyr	Phe	Thr	Ser	Leu	Phe	Pro	Tyr	Ala	Val	Leu	Thr		
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Ile	Phe	Phe	Val	Arg	Gly	Ile	Thr	Leu	Pro	Gly	Ser	Ser	Asp	Gly	Ile		
			260					265					270				
Leu	His	Met	Tyr	Lys	Pro	Lys	Leu	Glu	Lys	Leu	Leu	Asp	Pro	Thr	Val		
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Trp	Leu	Asp	Ala	Ala	Thr	Gln	Val	Phe	Tyr	Ser	Phe	Gly	Leu	Ala	Phe		
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Gly	Ser	Leu	Ile	Ala	Phe	Gly	Ser	Tyr	Asn	Pro	Pro	Asn	Asn	Asn	Cys		
305					310					315					320		
Val	Arg	Asp	Val	Leu	Leu	Val	Ser	Val	Cys	Asn	Ala	Leu	Thr	Ala	Ile		
				325					330					335			
Tyr	Ala	Ser	Val	Val	Ile	Phe	Ser	Ile	Leu	Gly	Phe	Lys	Ala	Tyr	Thr		
			340					345					350				
Met	Val	Glu	Asn	Cys	Ile	Val	Lys	Glu	Ile	Lys	Val	Leu	Ala	Leu	His		
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His	Ile	Gly	Gly	Phe	Thr	Leu	Asn	Ser	Thr	Ala	Asp	Tyr	Tyr	Arg	Glu		
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Gln	Phe	Pro	Arg	Leu	Asn	Gly	Thr	Ala	Ile	Ala	Ala	Leu	Asn	Leu	Thr		
385					390					395					400		
Gly	Cys	Thr	Met	Ser	Arg	Gln	Leu	Glu	Glu	Ala	Ala	Glu	Gly	Thr	Gly		
				405					410					415			

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 Pro Phe Trp Ser Ile Ile Phe Phe Leu Met Leu Leu Ser Leu Gly Leu
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 Glu Tyr Trp Leu Lys Met Phe Asp Ser Phe Ala Gly Thr Ile Gly Leu
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 Val Val Val Ala Leu Leu Lys Met Ile Ala Val Ile Tyr Ile Tyr Gly
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 Gly Ile Tyr Trp Gln Val Thr Trp Arg Tyr Val Gly Pro Ala Ile Val
 545 550 555 560
 Thr Cys Ile Leu Leu Ser Ser Leu Val Phe Met Leu Ile Asn Pro Pro
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 Met Tyr Gly Ala Trp Asn Ala Asp Glu Gly Arg Val Ile Lys Thr Pro
 580 585 590
 Tyr Pro Thr Trp Val Leu Val Ile Ala Val Leu Met Ile Leu Ala Gly
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 Val Leu Pro Ile Pro Val Val Leu Leu Leu Arg Arg Phe Gln Cys Leu
 610 615 620
 Ala Phe Asp Val Asp Ile His Gln Gly Ser Ile Arg Arg Ile Glu Thr
 625 630 635 640
 Thr Val Ser Thr Lys Glu Met Met Ser Asp Gln Asp Asn Val Glu Ser
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 Arg Pro Lys Lys
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<210> 13
 <211> 3513
 <212> DNA
 <213> Manduca sexta

 <220>
 <223> GABA transporter

<400> 13

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 <212> PRT
 <213> Manduca sexta

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 <223> GABA transporter

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 35 40 45
 Ile Gly Leu Ala Ile Gly Leu Gly Asn Val Trp Arg Phe Pro Tyr Leu
 50 55 60
 Cys Tyr Lys Asn Gly Gly Gly Ala Phe Leu Ile Pro Tyr Phe Leu Thr
 65 70 75 80
 Leu Phe Leu Ala Gly Ile Pro Met Phe Phe Met Glu Leu Ala Met Gly
 85 90 95
 Gln Met Leu Thr Ile Gly Gly Leu Gly Val Phe Lys Ile Ala Pro Ile
 100 105 110
 Phe Lys Gly Ile Gly Tyr Ala Ala Ala Val Met Ser Cys Trp Met Asn
 115 120 125
 Val Tyr Tyr Ile Val Ile Leu Ala Trp Ala Ile Phe Tyr Phe Phe Met
 130 135 140
 Ser Met Arg Ser Asp Val Pro Trp Arg Asn Cys Asp Asn Tyr Trp Asn
 145 150 155 160
 Thr Ala Thr Cys Val Asn Pro Tyr Asp Arg Lys Asn Leu Thr Cys Trp
 165 170 175
 Ser Ser Leu Gly Asp Met Ser Thr Phe Cys Thr Leu Asn Gly Arg Asn
 180 185 190
 Val Ser Lys Ala Val Leu Ser Asp Pro Val Lys Glu Phe Trp Glu Arg
 195 200 205
 Arg Ala Leu Gln Ile Ser Ser Gly Ile Glu His Ile Gly Asn Ile Arg
 210 215 220
 Trp Glu Leu Ala Gly Thr Leu Leu Leu Val Trp Val Leu Cys Tyr Phe
 225 230 235 240
 Cys Ile Trp Lys Gly Val Arg Trp Thr Gly Lys Val Val Tyr Phe Thr
 245 250 255
 Ala Leu Phe Pro Tyr Phe Leu Leu Thr Val Leu Leu Ile Arg Gly Ile
 260 265 270

Thr	Leu	Pro	Gly	Ala	Met	Glu	Gly	Ile	Lys	Phe	Tyr	Val	Met	Pro	Asn	275	280	285
Met	Ser	Lys	Leu	Leu	Glu	Ser	Glu	Val	Trp	Ile	Asp	Ala	Val	Thr	Gln	290	295	300
Ile	Phe	Phe	Ser	Tyr	Gly	Leu	Gly	Leu	Gly	Thr	Leu	Val	Ala	Leu	Gly	305	310	315
Ser	Tyr	Asn	Lys	Phe	Thr	Asn	Asn	Val	Tyr	Lys	Asp	Ala	Leu	Ile	Val	325	330	335
Cys	Ser	Val	Asn	Ser	Ser	Thr	Ser	Met	Phe	Ala	Gly	Phe	Val	Ile	Phe	340	345	350
Ser	Val	Val	Gly	Phe	Met	Ala	His	Glu	Gln	Gln	Arg	Pro	Val	Ala	Glu	355	360	365
Val	Ala	Ala	Ser	Gly	Pro	Gly	Leu	Ala	Phe	Leu	Ala	Tyr	Pro	Ser	Ala	370	375	380
Val	Leu	Gln	Leu	Pro	Gly	Ala	Pro	Leu	Trp	Ser	Cys	Leu	Phe	Phe	Phe	385	390	395
Met	Leu	Leu	Leu	Ile	Gly	Leu	Asp	Ser	Gln	Phe	Cys	Thr	Met	Glu	Gly	405	410	415
Phe	Ile	Thr	Ala	Val	Ile	Asp	Glu	Trp	Pro	Lys	Leu	Leu	Arg	Arg	Arg	420	425	430
Lys	Glu	Ile	Phe	Ile	Ala	Ile	Thr	Cys	Ile	Ile	Ser	Tyr	Leu	Val	Gly	435	440	445
Leu	Ser	Cys	Ile	Ser	Glu	Gly	Gly	Met	Tyr	Val	Phe	Gln	Ile	Leu	Asp	450	455	460
Ser	Tyr	Ala	Val	Ser	Gly	Phe	Cys	Leu	Leu	Phe	Leu	Ile	Phe	Phe	Glu	465	470	475
Cys	Val	Ser	Ile	Ser	Trp	Ala	Phe	Gly	Val	Asn	Arg	Phe	Tyr	Asp	Gly	485	490	495
Ile	Lys	Glu	Met	Ile	Gly	Tyr	Tyr	Pro	Thr	Ile	Trp	Trp	Lys	Phe	Cys	500	505	510
Trp	Val	Gly	Phe	Thr	Pro	Ala	Ile	Cys	Ile	Ser	Val	Phe	Ile	Phe	Asn	515	520	525
Leu	Val	Gln	Trp	Thr	Pro	Ile	Lys	Tyr	Met	Asn	Tyr	Glu	Tyr	Pro	Trp	530	535	540
Trp	Ser	His	Ala	Phe	Gly	Trp	Phe	Thr	Ala	Leu	Ser	Ser	Met	Leu	Cys	545	550	555
Ile	Pro	Gly	Tyr	Met	Ile	Tyr	Leu	Trp	Arg	Val	Thr	Pro	Gly	Thr	Trp	565	570	575
Gln	Glu	Lys	Phe	His	Lys	Ile	Val	Arg	Ile	Pro	Glu	Asp	Val	Pro	Ser	580	585	590

Leu Arg Thr Lys Met
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<212> DNA
<213> Aedes aegypti

<220>
<223> LAT transporter

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gatctgtttt catcaattga caaaatttta gatcagtgc aaatatgttt ggagtcgatt 1860
ttggatcata cactcccacg gttttttgtt gcgatgaaat cgcgaaatca ttagtcaaaa 1920
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atctagaagc aaaacatctc actgaaagag ggaaagacaa aagataagac tattatacat 2340
acacaaacac tcgaataaag caaactgctc gtagttagcc gttgaagtta gcatagtgcg 2400
agtatggaag ttttgaatag aaacgtaaga gattgaataa catagggttaa gtttgcaagc 2460
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aaaaaaaaa 2529
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<210> 16
 <211> 517
 <212> PRT
 <213> Aedes aegypti

<220>
 <223> LAT transporter

<400> 16
 Met Val Leu Lys Gln Arg Gly Ala Ala Ile Glu Leu His Ser Pro Thr
 1 5 10 15
 Glu Asp Val Leu Val Ser Pro Gly Thr Glu Ser Leu Pro Pro Ile Glu
 20 25 30
 Asn Gly Ala Ile Ala Gly Ser Gly Thr Ile Asp Gly Gly Gly Gly Asn
 35 40 45
 Glu Arg Val Lys Met Lys Lys Glu Leu Gly Leu Leu Glu Gly Val Ala
 50 55 60
 Ile Ile Leu Gly Ile Ile Phe Gly Ser Gly Ile Phe Ile Ser Pro Lys
 65 70 75 80
 Gly Val Leu Gln Glu Val Gly Ala Val Gly Thr Ser Leu Val Ile Trp
 85 90 95
 Val Thr Cys Gly Leu Leu Ser Met Ile Gly Ala Leu Cys Tyr Ala Glu
 100 105 110
 Leu Gly Thr Ala Ile Pro Lys Ser Gly Gly Asp Tyr Ala Tyr Ile Tyr
 115 120 125
 Glu Ala Tyr Gly Pro Leu Ser Ala Phe Leu Tyr Leu Trp Asp Ala Thr
 130 135 140
 Val Ile Phe Val Pro Ser Thr Asn Ala Ile Met Gly Leu Thr Phe Ala
 145 150 155 160
 Ser Tyr Val Phe Gln Pro Leu Phe Ala Ala Gly Cys Ser Val Pro Thr
 165 170 175
 Ile Gly Leu Gln Leu Phe Ala Ala Val Thr Ile Cys Leu Leu Thr Tyr
 180 185 190
 Ile Asn Ala Tyr Asp Val Arg Val Thr Thr Lys Met Gln Asn Val Phe
 195 200 205
 Met Phe Thr Lys Ile Gly Ala Leu Val Leu Val Ile Ile Val Gly Val
 210 215 220
 Val Trp Met Ser Leu Gly Gly Thr Glu Asn Phe Glu Asn Ala Phe Glu
 225 230 235 240
 Asn Thr Glu Thr Asp Pro Gly Lys Leu Ala Val Ala Phe Tyr Ser Gly
 245 250 255
 Ile Phe Ser Tyr Ala Gly Trp Asn Tyr Leu Asn Phe Met Thr Glu Glu
 260 265 270

Leu Arg Asp Pro Tyr Lys Asn Leu Pro Arg Ala Ile Tyr Ile Ser Leu
 275 280 285
 Pro Leu Val Thr Gly Ile Tyr Val Leu Ala Asn Met Ala Tyr Val Ala
 290 295 300
 Val Leu Ser Pro Gln Gln Ile Leu Ser Ser Asp Ala Ile Ala Val Thr
 305 310 315 320
 Phe Ala Gln Lys Ala Met Gly Trp Gly Ala Phe Val Met Pro Ile Leu
 325 330 335
 Val Ala Ile Ser Ala Phe Gly Gly Leu Ser Val His Ile Met Thr Ser
 340 345 350
 Ser Arg Met Cys Phe Val Gly Ala Arg Asn Gly His Met Pro Glu Ile
 355 360 365
 Leu Phe His Ile Asn Val Asn Arg Tyr Thr Ser Met Pro Ser Leu Val
 370 375 380
 Phe Leu Cys Leu Leu Ser Leu Leu Tyr Leu Phe Ile Ser Asp Val Tyr
 385 390 395 400
 Val Leu Ile Thr Tyr Ser Ser Ile Val Glu Ser Phe Phe Ile Met Leu
 405 410 415
 Ser Val Ser Ala Val Leu Tyr Phe Arg Tyr Thr Arg Pro Asp Ile Asn
 420 425 430
 Arg Pro Ile Lys Val Gln Leu Trp Val Pro Thr Leu Phe Val Ile Ile
 435 440 445
 Cys Ala Phe Leu Ile Val Val Pro Cys Tyr Val Ala Pro Tyr Glu Val
 450 455 460
 Gly Met Gly Val Leu Leu Thr Leu Ala Gly Ile Pro Val Tyr Tyr Val
 465 470 475 480
 Gly Val Ala Trp Lys Asn Lys Pro Glu Ser Phe Glu Asn Val Leu Arg
 485 490 495
 Arg Ala Thr Gln Phe Cys Gln Lys Met Phe Met Thr Ala Lys Glu Glu
 500 505 510
 Asn Asp Asp Glu Glu
 515

<210> 17

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:1S forward
degenerate primer for NTTs (A69)

<220>
 <221> modified_base
 <222> (19)
 <223> n = i

 <220>
 <221> modified_base
 <222> (25)
 <223> n = i

 <220>
 <221> modified_base
 <222> (31)
 <223> n = g, a, c or t

 <400> 17
 cggaattctg gscaayrtnt ggmgnattycc nta

33

<210> 18
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:4A reverse
 degenerate primer for NTTs (A67)

<220>
 <221> modified_base
 <222> (24)..(25)
 <223> n = i

<220>
 <221> modified_base
 <222> (28)
 <223> n = i

<220>
 <221> modified_base
 <222> (34)
 <223> n = g, a, c or t

<400> 18
 gccaaagcttg aagaagatyt grgnngcngc rtcnabcca

39

<210> 19
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:2S reverse
 degenerate primer for NTTs (A70)

<220>
 <221> modified_base
 <222> (16)
 <223> n = i

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<220>
<221> modified_base
<222> (19)
<223> n = i

<220>
<221> modified_base
<222> (22)
<223> n = i

<220>
<221> modified_base
<222> (25)
<223> n = g, a, c or t

<400> 19
ctccatggar aayggnggng gngcntt

```

27

```

<210> 20
<211> 30
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:3A reverse
degenerate primer for NTTs (A68)

```

```

<220>
<221> modified_base
<222> (13)
<223> n = i

```

```

<220>
<221> modified_base
<222> (16)
<223> n = i

```

```

<220>
<221> modified_base
<222> (19)
<223> n = i

```

```

<220>
<221> modified_base
<222> (22)
<223> n = i

```

```

<220>
<221> modified_base
<222> (25)
<223> n = g, a, c or t

```

```

<220>
<221> modified_base
<222> (28)
<223> n = g, a, c or t

```

```

<400> 20
ggcgagctcg gncncggna gngtnrcncc

```

30